ELabELN | Template Use Case White Paper

DNA Extraction Experiment Template

Structured Documentation for Silica-Column Genomic DNA Isolation — From Cell Pellet Through Yield and A260/A280 Purity QC

APPLIES TO

- Academic and life sciences research laboratories
- Biotechnology and molecular biology R&D groups
- Core genomics, molecular biology, and biobanking facilities
- Diagnostics laboratories and contract research organizations (CROs)

RELEVANT COMPLIANCE & INTEGRITY FRAMEWORKS

- FDA 21 CFR Part 11 — Electronic records and signatures
- EU Annex 11 — Computerized systems in regulated environments
- GAMP 5 — Software validation for regulated industries
- NIH / NSF reproducibility and data-management requirements

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1. Executive Summary

A DNA extraction is only as valuable as what comes after it. The genomic DNA a lab isolates today becomes the input to a PCR, a sequencing run, a genotyping assay, or a frozen bank tomorrow — and if the yield is too low or the purity is off, that downstream work fails or, worse, produces misleading results. The extraction is the classic “garbage in, garbage out” step: an eluate contaminated with residual ethanol, salt, or protein can sail through a spectrophotometer reading and still ruin an enzymatic reaction days later. Yet the values that predict all of this — input mass, elution volume, concentration, and the A260/A280 and A260/A230 purity ratios — are the ones most often scribbled on a tube or lost in free text.

The ELabELN DNA Extraction Experiment Template solves this by providing a pre-built, fully structured prep record that loads from the template library in a single click. It ships with a 10-step silica-column protocol, validated kit references, pre-wired purity QC fields, and typed inputs for sample source, input mass, elution volume, yield in nanograms per microliter, and both purity ratios. Kit lots, column batches, and Proteinase K aliquots link to the ELabELN inventory, and the tamper-evident audit trail captures every step check-off, every measurement, and every electronic signature.

This white paper describes what the template contains, the prep use case it is designed to support, the upstream and downstream workflows it connects to, the benefits it delivers to the scientist, and how a laboratory can deploy it and begin extracting within days.

> **KEY BENEFIT**
> Labs that adopt the DNA extraction template stop re-recording the same protocol in free text, capture kit-lot and column-batch traceability automatically, and build a queryable yield-and-purity history across preps that pinpoints a bad kit lot or sample-handling step before it wastes a downstream experiment — all in an audit-ready record.

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2. What Is DNA Extraction, and Why Does Documentation Matter?

2.1 The Technique

Silica-column DNA extraction isolates genomic DNA from a biological sample through a lyse–bind–wash–elute sequence. Cells are lysed and their proteins digested with Proteinase K at 56 °C; ethanol is added to create binding conditions; the lysate is passed through a silica-membrane spin column that captures DNA while contaminants flow through; two washes (AW1 and AW2) remove residual protein, salt, and other impurities; and the purified DNA is eluted in a low-salt buffer or nuclease-free water. The eluate is then quantified — by NanoDrop or Qubit — and its purity assessed from the ratio of absorbance at 260 nm (nucleic acid) to 280 nm (protein) and 230 nm (organics and salts).

Extraction is the routine front end of genomics: preps feed PCR and qPCR, Sanger and next-generation sequencing, genotyping assays, and long-term DNA banks. Two numbers decide whether a prep is fit for that purpose. Yield — concentration times elution volume — determines whether there is enough material; purity — an A260/A280 near 1.8 and an A260/A230 near 2.0–2.2 for clean DNA — determines whether contaminants will inhibit the downstream reaction. A low A260/A230, for example, signals guanidine or ethanol carryover that can quietly inhibit a PCR.

Because the eluate looks identical whether it is clean or contaminated, **the purity and yield numbers — and the reagent lots behind them — are the only reliable predictor of downstream success, which is exactly why they must be captured, not remembered.**

2.2 The Documentation Problem

Recording extractions in a paper notebook or ad-hoc spreadsheet creates a set of interconnected risks:

- Yield and purity ratios are jotted on a tube or a printout, so the QC that predicts downstream success is never assembled into a comparable record.
- Kit lot, column batch, and Proteinase K aliquot are not recorded, so a bad reagent lot cannot be identified when a run of preps underperforms.
- Input mass, lysis time, and elution volume live in free text, where they cannot be queried or compared across preps.
- The extraction is disconnected from the downstream PCR or sequencing experiment, so a failed reaction cannot be traced back to a marginal prep.
- There is no timestamped, attributed record of who ran which prep and when — a baseline requirement for shared projects and regulated work.
- Prior preps from a sample type or kit lot cannot be retrieved, so the yield-trend that would flag a declining kit is invisible.

These are the gaps that let a marginal prep sabotage downstream work, and they are the gaps this template was designed to close.

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3. Template Overview: What Ships with the Template

The ELabELN DNA Extraction Experiment Template is a pre-populated experiment record available to all ELabELN subscribers directly from the template library. It ships configured for genomic DNA isolation from cultured mammalian cells (HEK293) using a silica-membrane spin-column workflow, with a 10-step protocol covering cell-pellet harvest through final elution and Qubit-based concentration confirmation. The default configuration assumes a Qiagen DNeasy Blood & Tissue Kit (or equivalent silica-column chemistry), Proteinase K digestion at 56 °C, ethanol-based binding, two column washes (AW1 + AW2), and elution in low-salt AE buffer or nuclease-free water. Every section is editable — the configuration is a tested baseline, not a locked format.

3.1 Template Sections at a Glance

The template populates the existing ELabELN experiment sections your lab already works in. Your team edits a working baseline instead of recording the same protocol in free text every time.

Section	What it pre-populates
Main Text	Protocol summary, sample-source notes, and the expected yield range, authored in the TinyMCE rich-text editor and linked to the downstream PCR experiment.
Extra Fields	Ten structured, typed fields grouped as Sample, Lysis, and Elution & QC — cell line or tissue source, input mass or cell count, lysis temperature and duration, elution volume, eluate concentration (ng/µL), A260/A280 ratio, and A260/A230 ratio. Typed values make QC outcomes queryable across preps.
Steps	A 10-step workflow checklist covering cell harvest through Qubit concentration confirmation, with spin times pre-filled. Each tick is timestamped to the audit trail.
Compounds	Spin-column kit, Proteinase K, AW1/AW2 wash buffers, AE elution buffer, and ethanol pre-linked from the compound database, with kit lot and column batch carried in automatically.
Links & Resources	Pre-wired to the lab's gDNA Extraction SOP v2.1, the DNeasy kit-insert reference, and downstream PCR experiments.
Storage & Files	−20 °C eluate storage and source cell-pellet storage, plus labelled attachment slots for NanoDrop and Qubit measurement files (CSV + PDF).

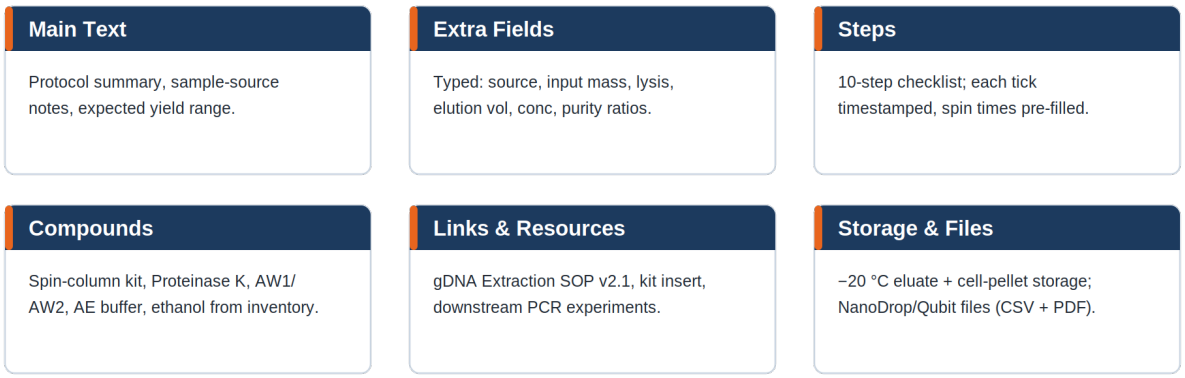
Main Text
Protocol summary, sample-source notes, expected yield range.
Extra Fields
Typed: source, input mass, lysis, elution vol, conc, purity ratios.
Steps
10-step checklist; each tick timestamped, spin times pre-filled.
Compounds
Spin-column kit, Proteinase K, AW1/AW2, AE buffer, ethanol from inventory.
Links & Resources
gDNA Extraction SOP v2.1, kit insert, downstream PCR experiments.
Storage & Files
−20 °C eluate + cell-pellet storage; NanoDrop/Qubit files (CSV + PDF).

Figure 1. The six ELabELN experiment sections pre-populated by the DNA extraction template.

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3.2 The 10-Step Protocol

The workflow checklist is the operational spine of the template. Each step maps to a discrete bench action and writes a timestamped, user-attributed entry to the audit trail when checked off — with the final quantify and QC steps capturing the yield and purity values that determine whether the prep is fit for downstream use.

Step	Action	What it captures
1	Harvest cell pellet	Sample source; input mass / cell count
2	Lyse (Proteinase K, 56 °C)	Lysis temperature and duration
3	Add ethanol	Binding conditions
4	Bind to column	Silica-membrane capture
5	Wash 1 (AW1)	—
6	Wash 2 (AW2)	—
7	Dry spin	Residual-ethanol removal
8	Elute (AE buffer / water)	Elution volume
9	Quantify	Concentration (ng/µL) by NanoDrop / Qubit
10	QC & store	A260/A280, A260/A230; −20 °C; e-signature

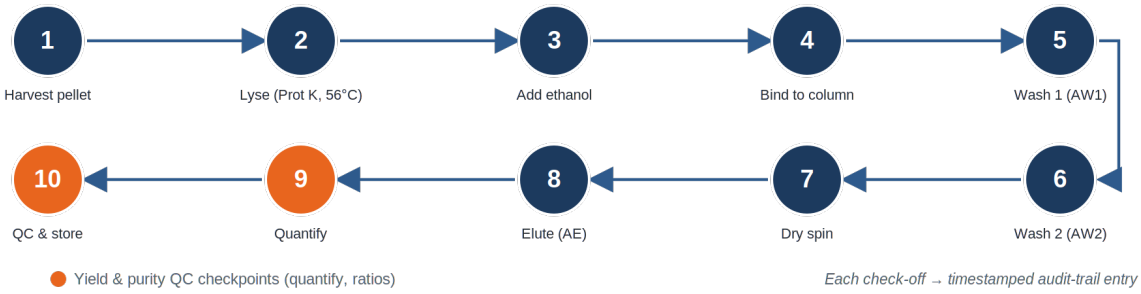

Figure 2. The 10-step silica-column workflow — orange steps are the yield and purity QC checkpoints; every check-off writes a timestamped entry to the ELabELN audit trail.

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4. The Use Case: When and How the Template Is Used

The template is intended as a tested baseline for academic and life sciences labs running genomic DNA preps for downstream molecular work. It is configured around a recognizable reference — a silica-column gDNA prep from HEK293 cells — but the scenarios it serves span the whole genomics front end.

4.1 gDNA for PCR and qPCR (Primary Use Case)

The most common scenario: extracting template DNA for amplification. The template captures the yield and purity of the eluate and links to the downstream PCR experiment, so a reaction that fails can be traced directly to the prep that fed it — and a prep with a marginal A260/A230 is flagged before it inhibits an amplification.

4.2 Sequencing Preparation

Sanger and next-generation sequencing both demand DNA of defined concentration and purity. The template's typed QC fields document that the input met specification, and the record links forward to the sequencing workflow — connecting the prep to the read it enabled.

4.3 Genotyping

Genotyping assays run across many samples, where consistency is everything. The queryable yield and purity fields let a lab confirm that every sample in a genotyping batch met the same QC bar, rather than discovering an outlier prep after the assay.

4.4 DNA Banking and Biobanking

Banked DNA must carry its provenance for years. The template records the sample source, the reagent lots, the yield and purity at banking, and the −20 °C storage location, so an archived eluate remains fully documented whenever it is retrieved.

4.5 Kit and Sample QC: Yield-Trend Analysis

Because concentration, total yield, and purity ratios are typed values, the template doubles as a running quality-control record for kits and sample handling. A lab can pull every prep from a specific cell line or kit lot, compare yield and purity, and make an evidence-based call on when to revisit a problematic kit batch or a sample-handling step — rather than absorbing a slow decline unnoticed.

4.6 Multi-User, Multi-PI, and CRO Settings

Because every ELabELN edition includes unlimited users, the PI, postdocs, students, and visiting collaborators can all run preps from the same template, and the pre-wired SOP enforces one consistent procedure. Granular permissions let the PI decide who may edit extractions versus only review them — the basis a CRO needs to standardize prep documentation across client studies.

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5. Dependencies and Connected Workflows

The DNA extraction template does not exist in isolation. It sits inside a network of connected workflows — upstream, parallel, and downstream — that give the prep record its full scientific and provenance value.

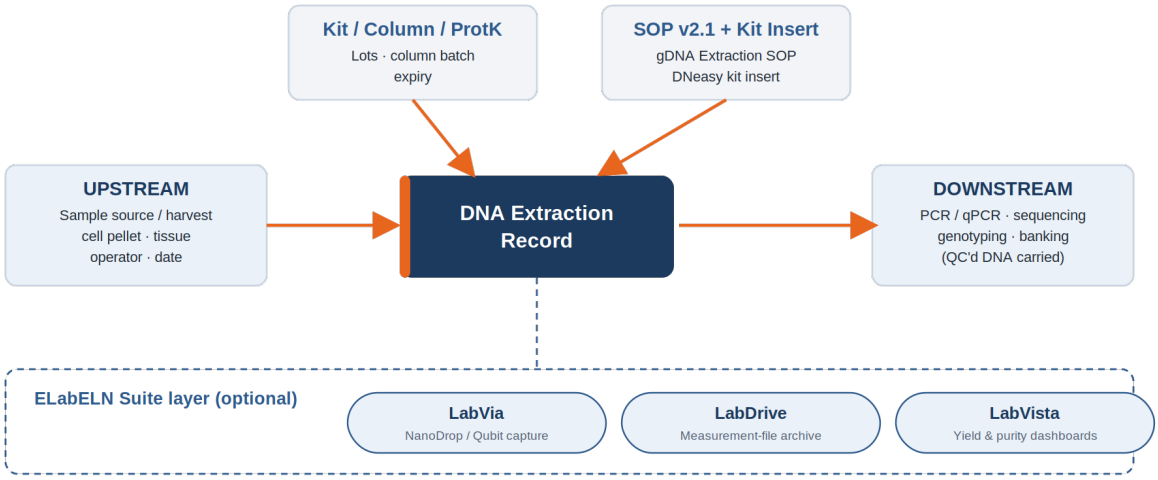

Figure 3. The template connects an upstream sample source, parallel kit and SOP systems, and downstream PCR, sequencing, genotyping, and banking workflows.

5.1 Upstream: Sample Source and Harvest

Every prep begins with a sample — a cell pellet, a tissue, blood, or another source. The template records the source and input mass, so opening a prep surfaces exactly what went in, the operator, and the date — anchoring the eluate's provenance to the material it came from.

5.2 Parallel: Kit, Column, and Reagent Inventory

The Compounds section links the spin-column kit, Proteinase K, AW1/AW2 wash buffers, AE elution buffer, and ethanol directly to the ELabELN inventory. Because kit and column performance drift lot to lot, this traceability is what makes yield problems diagnosable. Through the link the record automatically carries:

- **Kit lot and column batch**, so a run of low-yield preps can be pinned to a specific lot rather than guessed at.
- **Expiry and stock levels**, with low-stock warnings before a run, so a prep is not started against an expired or depleted kit.
- **Full reagent traceability for downstream work**, so the DNA feeding an experiment carries the lot provenance of the prep that produced it.

Barcode and QR scanning can populate these links from the physical kit box, keeping lot capture effortless.

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5.3 Parallel: SOPs and the Kit Insert

The Links section connects the prep to the lab's version-controlled gDNA Extraction SOP (v2.1 by default) and to the DNeasy kit-insert reference. Because the SOP is version-controlled, every prep records which procedure version it followed, and the kit insert documents the exact chemistry the run assumes.

5.4 Downstream: PCR, Sequencing, Genotyping, and Banking

The extracted DNA is an input, not an endpoint. The template links forward to the experiments the eluate feeds — PCR and qPCR, Sanger and NGS sequencing, genotyping, and long-term banking — and the spreadsheet editor captures the NanoDrop or Qubit concentration with calculated total yield, supporting yield-trend analysis across sample batches. Because the QC values are typed and queryable, a downstream experiment can confirm that its template met specification before the reaction is set up.

5.5 The ELabELN Suite: Instruments and Dashboards

Everything above is available in ELabELN Standard. Labs on the ELabELN Suite gain three layers that connect to the same record: LabVia captures data directly from quantification instruments such as NanoDrop and Qubit; LabDrive adds metadata search, versioning, and role-based access across measurement-file archives and other lab files; and LabVista builds yield and purity dashboards and trends on the structured prep metadata. The same audit trail and data-integrity controls span all layers.

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6. How the Scientist Benefits

The template is built to deliver value at the bench, not just to the quality system. The benefits compound with every prep a lab runs.

6.1 Start From a Tested Baseline, Not Free Text

The scaffold — protocol with spin times pre-filled, typed fields, kit and reagent links, SOP and kit insert — is already built. The scientist edits a working configuration to match the sample and kit they actually run, rather than re-recording the same protocol in free text every time. The first prep is faster, and every subsequent one is consistent with it.

6.2 Document by Doing

Checking off each of the 10 steps as it happens produces a contemporaneous, timestamped record as a by-product of the prep. Spin times are pre-filled, and there is no separate write-up to reconstruct later.

6.3 Never Lose Kit-Lot Provenance Again

Because the kit, columns, and Proteinase K are linked to inventory, the lot and batch numbers are captured automatically and permanently on every prep. When a run of preps underperforms, the reagent-lot history is on the record — closing the most common extraction troubleshooting gap by default.

6.4 A Queryable Yield-and-Purity History

Typed concentration, yield, and purity-ratio fields make QC queryable. A scientist can pull every prep from a sample type or kit lot, compare yield and both purity ratios at a glance, and catch a declining kit or a sample-handling problem early — instead of discovering it downstream.

6.5 Protect Downstream Work with Audit-Ready Records

The tamper-evident audit trail, version-controlled SOP linkage, and electronic signatures mean the record that results from normal use is already structured to support reproducibility documentation, multi-PI collaboration, and FDA 21 CFR Part 11 review when the lab's quality system requires it — so a marginal prep can no longer silently undermine the PCR, sequencing, or genotyping that depends on it.

> **AT THE BENCH, IN PRACTICE**
> A student opens the template, sets the sample source and kit to match today's prep, scans the kit box to capture its lot and column batch, and checks off each step as the extraction proceeds. At the quantify step, the NanoDrop concentration and the A260/A280 and A260/A230 ratios go straight into typed fields, total yield is calculated, and the measurement PDF attaches to the record. Weeks later, when a downstream PCR underperforms, the PI pulls the prep and sees at a glance that the A260/A230 was marginal — and which kit lot produced it.

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7. Yield, Purity, and QC Tracking

7.1 The Default Reference: HEK293 gDNA on a Silica Column

The template ships configured to extract genomic DNA from HEK293 cells using a DNeasy-style silica-column kit, with Proteinase K lysis at 56 °C and elution in AE buffer. Quantification is by NanoDrop or Qubit, and purity is read from the A260/A280 ratio (near 1.8 for clean DNA; lower indicates protein or phenol carryover) and the A260/A230 ratio (near 2.0–2.2; lower indicates salt, guanidine, or ethanol carryover). This concrete reference demonstrates the full prep-and-QC workflow out of the box; swap the sample source, kit chemistry, or elution volume to match what your lab runs.

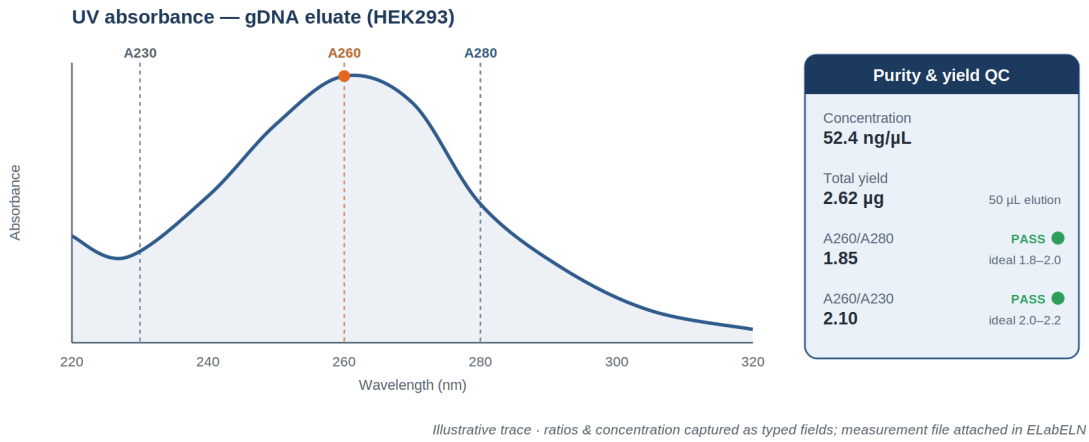

Figure 4. A NanoDrop-style UV absorbance trace with the derived concentration and purity ratios checked against acceptance ranges. Illustrative trace; the ratios and concentration are captured as typed fields and the measurement file is attached in ELabELN.

7.2 How the Template Handles Yield and Purity

The concentration (NanoDrop or Qubit), the A260/A280 ratio, and the A260/A230 ratio are captured as typed fields on every prep, and the spreadsheet editor calculates total yield from the concentration and elution volume. The measurement files (CSV and PDF) attach to the same record. Because all of these are typed and queryable, a lab can compare yield and purity across preps — by sample type or by kit lot — and treat the extraction record as a running QC log rather than a set of isolated readings.

Element	Default configuration	Editable to
Sample source	Cultured mammalian cells (HEK293)	Tissue, blood, plant, FFPE, saliva, bacterial pellet
Kit chemistry	Silica spin column (DNeasy)	Magnetic bead, phenol-chloroform, salting-out
Lysis	Proteinase K, 56 °C	Any input mass / lysis time
Elution	AE buffer or nuclease-free water	Any elution volume
Quantification	NanoDrop / Qubit; A260/A280, A260/A230	Any QC readout

Figure 5. The template's default configuration — fully editable for any sample source, kit chemistry, or elution scheme.

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8. Configuring the Template for Your Prep

Adapting the template to a different sample or kit is a matter of editing the relevant sections — not rebuilding the structure.

8.1 Change the Sample Source

Swap in tissue, blood, plant material, FFPE, saliva, or bacterial pellets as the sample source. The Sample, Lysis, and Elution & QC field groups apply across all of them; adjust the input mass and lysis parameters to suit.

8.2 Swap the Kit Chemistry

Change the extraction chemistry — silica column, magnetic bead, phenol-chloroform, or salting-out. If the kit and reagents already exist in the ELabELN compound database, simply re-link them; their lot and batch numbers flow in automatically.

8.3 Adjust Input, Lysis, and Elution

Edit the input mass or cell count, the lysis temperature and duration, and the elution volume to match your protocol and the downstream workflow — a smaller elution volume for a higher concentration, a larger one for a gentler, more dilute eluate.

8.4 Save a Custom Version

Once configured, save your edits as a private template scoped to your lab, or publish back to the ELabELN template library. Every subsequent prep of that sample type opens from your configured version, and separate versions can be maintained for different sample sources, kits, or regulatory contexts.

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9. Getting Started

ELabELN Standard is a cloud-hosted SaaS deployment typically live within one to two business days of account creation. There is no hardware to buy, no IT project, and no per-seat licensing.

1. **Start an ELabELN account.** Visit elabeln.com/get-started. ELabELN Standard runs on LabLynx's managed cloud infrastructure.
2. **Provision your instance.** LabLynx provisions the instance within one to two business days; you receive a URL, admin credentials, and onboarding documentation.
3. **Load the DNA extraction template.** From the template library, select the DNA extraction template and click “Use This Template.” An editable instance opens immediately.
4. **Add your kits and reagents to the inventory.** Enter your extraction kits, Proteinase K, wash and elution buffers, and ethanol with lot numbers, column batches, and expiry, and record −20 °C eluate storage locations. This is a one-time setup step.
5. **Link your SOP and kit insert.** Upload your extraction SOP and the kit insert, and connect them to the template's Links section.
6. **Customize the template for your sample.** Edit the sample source, kit chemistry, input mass, lysis parameters, and elution volume, then save as a private team version.
7. **Run your first prep.** Open your saved template, complete the 10-step checklist, attach the NanoDrop or Qubit measurement, and have the PI sign off electronically.

> **TYPICAL TIMELINE**
> Day 1: Account requested at elabeln.com/get-started. Day 2–3: Instance provisioned; kit/reagent inventory populated; SOP and kit insert uploaded. Day 3–4: Template configured and saved as a private version for your sample type. Day 4–5: First prep documented in ELabELN with yield and purity captured and an e-signature.

9.1 ELabELN Standard vs. ELabELN Suite

Capability	Standard	Suite
DNA extraction template access	Included	Included
Unlimited users	Included	Included
Audit trail and e-signatures	Included	Included
Kit / column / reagent inventory with lot tracking	Included	Included
SOP & kit-insert linking with version control	Included	Included
NanoDrop / Qubit measurement attachments	Included	Included
LabVia direct NanoDrop / Qubit capture	—	Suite layer
LabDrive measurement-file archive search & versioning	—	Suite layer
LabVista yield & purity dashboards	—	Suite layer

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10. Frequently Asked Questions

Can I configure the template for my sample type and kit?

Yes. Every section is editable. Swap in tissue, blood, plant material, FFPE, saliva, or bacterial pellets as the sample source. Change the kit chemistry (silica column, magnetic bead, phenol-chloroform, salting-out), adjust the input mass and lysis parameters, or switch to a different elution volume. Save your edits as a private template scoped to your lab, or publish back to the ELabELN template library.

Does the template work with RNA extractions too?

This template is configured specifically for genomic DNA extraction. RNA preps share the structural pattern — lyse, bind, wash, elute — but use different chemistries (TRIzol, on-column DNase digest, RNase-free buffers). The ELabELN RNA-Seq template covers the RNA extraction workflow; for plasmid DNA preps, the bacterial transformation template links downstream to a separate miniprep workflow.

How does the template track yield and purity over time?

The spreadsheet editor captures concentration (NanoDrop or Qubit) and the A260/A280 and A260/A230 purity ratios, with total yield calculated from the elution volume. Because the typed fields are queryable across preps, your lab can pull every prep from a specific cell line or kit lot and compare yield and purity — supporting decisions about when to revisit a problematic kit batch or sample-handling step.

Is it included in every ELabELN plan?

Yes. Every published template in the ELabELN library is available to all subscribers in both the Standard and Suite editions, with unlimited users in either edition and no per-template fee.

Can my whole lab use this template?

Yes. Every ELabELN edition includes unlimited users, so the PI, postdocs, grad students, rotating researchers, and visiting collaborators can all use the template without per-seat charges. Granular permissions let the PI control who can edit extractions versus only review them.

How quickly can my lab start extracting in ELabELN?

ELabELN Standard cloud deployment is typically live in one to two business days. Once the instance is provisioned, the template loads from the library in a single click, with the sample source, kit references, and elution parameters editable to match the preps your lab actually runs.

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11. Conclusion

The ELabELN DNA Extraction Experiment Template is not simply a digital version of a prep protocol. It is a structured, audit-ready, searchable record that connects to your kit and reagent inventory, your SOPs and kit inserts, the sample it came from, and the PCR, sequencing, genotyping, and banking workflows it feeds — and, in the Suite edition, your quantification instruments and yield dashboards. It turns the routine front end of genomics into a workflow whose quality is documented, comparable, and defensible.

For a laboratory that extracts DNA regularly, the benefit compounds with every prep. Yield and purity accumulate into one queryable QC history. Every kit lot and column batch is traceable. Every SOP version is documented. Every prep is timestamped, and every measurement is authenticated — so a marginal extraction can no longer quietly undermine the downstream work that depends on it, and a declining kit lot is caught before it costs an experiment.

The template is available to all ELabELN subscribers today. A new instance is live in one to two business days, and the first structured prep is typically complete within a week of account creation.

GET STARTED

Visit elabeln.com/get-started to request your ELabELN instance, or contact LabLynx at 866.522.5969 or info@lablynx.com. Load the DNA extraction template, configure it for your sample type and kit, and run your next prep from a tested, audit-ready baseline.

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